

EXHIBIT 2

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Section 1					
	(1)	1	10	20	30
AAH18130_PAR1L	(1)	-----	MRSPSAAWLLGAAILLASA	LSCSGTIQGTNRSSKGRSLIG	
NP_001983_PAR1	(1)	MGPRRLLLVAACFSLCGPLLSARTRAR	RPESKATNATLDPRSFL		
NP_835230_P2Y8	(1)	-	-	-	-
TransBD243560_HG52	(1)	-	-	-	-
NP_004092_PAR3	(1)	-	-	MKALIFAAAGLLLLPTFCQSGMENDTNNLAKPTLPIK	
NP_005287_P2Y9	(1)	-	-	-	-
P79928_XP2Y	(1)	-	-	-	-
Consensus	(1)	-	-	-	-
Section 2					
	(46)	46	60	70	80
AAH18130_PAR1L	(41)	-	-	KVDGTSHTVGKGVT	VETVFSVDE
NP_001983_PAR1	(46)	RNPNDKYEPFWEDEEKNESGLTEYRLVSINKSSPL	QQLPAFISE		
NP_835230_P2Y8	(1)	-	-	-	MQVPNSTGP
TransBD243560_HG52	(1)	-	-	-	DN
NP_004092_PAR3	(39)	TFRGAPPNSFEFPFSALEGWTGATITVKIKCP	-EESASHLHVKN		
NP_005287_P2Y9	(1)	-	-	MGDRRFIDFQFQDSNSSLR	PRLGNATA
P79928_XP2Y	(1)	-	-	MTEDIMATSYP	TFLTPYLP
Consensus	(46)	-	-	M	V
Section 3					
	(91)	91	100	110	120
AAH18130_PAR1L	(64)	F	SASVLTGKLTTVFLPIVYTIVEVVGLESNGMALWWFL	FRTKKHH	
NP_001983_PAR1	(91)	DASGYLTSSWLTLFVPSVYTGVEVVSLELNIMAI	VVFLIKMKVKK		
NP_835230_P2Y8	(12)	A	TQOMERNPAIAVALPVVYSLEVAAVSIEGNLF	SLWVLCRRMGPRS	
TransBD243560_HG52	(12)	A	TQOMERNPAIAVALPVVYSLEVAAVSIEGNLF	SLWVLCRRMGPRS	
NP_004092_PAR3	(83)	ATMGYLTSSLSTKLIPAIYLLVEVVGVBANAVT	EWMLFFTR-SI		
NP_005287_P2Y9	(28)	NNTCIVDDSFKYNLNGAVYSV	WEILGLITNSVSLFV	CFRMKMRS	
P79928_XP2Y	(32)	EDTCVFDEGFKF	LLLPVSYSAVEMVGELN	TAAMWIFIAKMRPWN	
Consensus	(91)	TL	ML	V	LPVVYSLVVVGLP NIMALWVF RMK R
Section 4					
	(136)	136	150	160	170
AAH18130_PAR1L	(109)	PAVIYMANLALADLTSVIWFPLKTA	YHIHGNNW	IYGGEALCNVALIG	
NP_001983_PAR1	(136)	PAVYVYMLHLATADVLEVS	VLPFKISYYFSGSDWQEGSEL	CRFVTA	
NP_835230_P2Y8	(57)	PSVIEMINLSVTDLMLASVL	PFQIYYHCN	RHHWVEGVLLCNVVT	
TransBD243560_HG52	(57)	PSVIEMINLSVTDLMLASVL	PFQIYYHCN	RHHWVEGVLLCNVVT	
NP_004092_PAR3	(127)	CTTVEYTNLAIAADF	LCVTEPFKIA	YHNGNNWVEGEVLCRATT	V
NP_005287_P2Y9	(73)	ETAI	EITNLAVSDLLEFVCT	CFKIEYNFN	-RHWPEGETLCKTSGT
P79928_XP2Y	(77)	PTTVYMFNLALS	DTLYVLS	PTLVYVYADKNNWPEGEN	LCLEVRF
Consensus	(136)	PTVIFM	NLAVALLLFV	LPFKIYYYH	N WVFGELLCKVVT

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Section 5

(181)	181	190	200	210	225
AAH18130_PAR1L (154)	FFYGNMYCSILFMTCLSMQRWVIVNIPMGHSRKK	-ANIAIGISLA			
NP_001983_PAR1 (181)	AFYCNMYASILLMTVISIDRFLAVVYPMOSLSWRTLGRASFTCLA				
NP_835230_P2Y8 (102)	AFYANMYSSILTMTTCISVERFLGVLYPLSSKRWRRRYAVAACAG				
TransBD243560_HG52 (102)	AFYANMYSSILTMTTCISVERFLGVLYPLSSKRWRRRYAVAACAG				
NP_004092_PAR3 (172)	IFYGNMYCSILLIACISINRYLAIVHPFTYRGLPKHTYALIVTCGL				
NP_005287_P2Y9 (117)	AFLTNIYGSMFLTCISVDRLAIVYPRFRSRTIRTRNSAIVCAG				
P79928_XP2Y (122)	LFYANLYSSILFLLTCISVHRYRGVCHPITSLLRMMNAKHAYVICAL				
Consensus (181)	AFYANMYSSIL MTCISVDRFLAVVYPLSSKR R RYAV CAG				

Section 6

(226)	226	240	250	260	270
AAH18130_PAR1L (198)	TWELLILVLTIPYVVKQIIFIPATNITTCHDVLPPEQLE	--VGDMF			
NP_001983_PAR1 (226)	TWALLAJAGVVPVLKEQIIQVPGINNITTCHDVLPNETLL	--EGYYA			
NP_835230_P2Y8 (147)	TWELLILTALSPIARTDLTYPVHALGIIITCFDVLKWTMILPSVAMWA				
TransBD243560_HG52 (147)	TWELLILTALSPIARTDLTYPVHALGIIITCFDVLKWTMILPSVAMWA				
NP_004092_PAR3 (217)	VWATVFLYMLPFFILKQEYLYVQPDITTCHDVHNTCES-SSPFQL				
NP_005287_P2Y9 (162)	VWILVLSGGISASLFPSTNVNNAT-TTCFEGFSKRW-KTYLS				
P79928_XP2Y (167)	VWLSVTLCVPNLITFVTVSPKVKN-TICHDTRPEDF-ARYV				
Consensus (226)	VWLLVL ALIPL I T V AL ITTCHDVLL A WA				

Section 7

(271)	271	280	290	300	315
AAH18130_PAR1L (241)	NYFLSIATGVFLFPAFLTAASAVLMIIRMLRSSAMDENS	--EKKR			
NP_001983_PAR1 (269)	YYFSAFSAVFFFVPLTISTVGVVSLIRCLSSSAVANRS	--KKS			
NP_835230_P2Y8 (192)	VFLFTIIFILLFIIPFVITVACYTATILKLLRTEEHGR	--EQRR			
TransBD243560_HG52 (192)	VFLFTIIFILLFIIPFVITVACYTATILKLLRTEEHGR	--EQRR			
NP_004092_PAR3 (261)	YYFISIATFGFLIPFVLIYCYAAIIRTLN--AYDHR--WLWY				
NP_005287_P2Y9 (203)	KITIFIEVVGFIIPLILNVGSSVVLRLTRKPATLSQI-GTNK				
P79928_XP2Y (207)	EYSTATMCGLFGIPCDTIAGCNGLMTRELMKPIVSGNQQTLPSYK				
Consensus (271)	Y SI ILLFLIP VITVACY AIIR L KS A R				

Section 8

(316)	316	330	340	350	360
AAH18130_PAR1L (283)	KRAIKLIVSVLAMYLICFTPSNLLELVVHYFLIKSQGQ	--SHV			
NP_001983_PAR1 (311)	--ALFISAAVFCIFIICFGPTNVLEIAHYSFLSHTST	--TEAA			
NP_835230_P2Y8 (234)	-RAVGLAAVVLIAEVTCFAAPNNFVLLAHIVSRLFYG	--KSY			
TransBD243560_HG52 (234)	-RAVGLAAVVLIAEVTCFAAPNNFVLLAHIVSRLFYG	--KSY			
NP_004092_PAR3 (300)	--VKASLLLILVIEITTCFAPSNIILITHANYYYNN	--TDGL			
NP_005287_P2Y9 (245)	KKVLEKMITVHMAVFVVCFVPYNSVLFYALVRSQAINTNCFLERFA				
P79928_XP2Y (252)	KRSIKTIIFVMIAFACFMPFHITRTEYYARLLGIK-CYALNVI				
Consensus (316)	RAVKLA VVLLIFVICFAP NIVLILHY R				

					Section 9	
	(361)	361	370	380	390	405
AAH18130_PAR1L	(323)	Y A L Y I V A L C Q L S T L N S C I D P E V Y Y F V S H D F R D H A K N A L L C R S V R				
NP_001983_PAR1	(350)	Y F A Y L L C V C V S S I S S C I D P L I Y Y Y A S S E C Q R Y V Y S I L C C K E S S D				
NP_835230_P2Y8	(272)	Y H V Y K L T L C L S C L N N C L D P E V Y Y F A S R E F Q L R L R E Y L G C R R V P R				
TransBD243560_HG52	(272)	Y H V Y K L T L C L S C L N N C L D P E V Y Y F A S R E F Q L R L R E Y L G C R R V P R				
NP_004092_PAR3	(337)	Y F I Y L I A L C I G S L N S C L D P F L Y E L M S K T R N H S T A Y L T K				
NP_005287_P2Y9	(290)	K I M Y P I T L C L A T L N C C F D P E I Y Y F T L E S P O K S F Y I N A H I R M E S L				
P79928_XP2Y	(296)	N V T Y K V T R P L A S A N S C I D E I L Y F L A N D R Y R R R L I R T V R R R S S V P N				
Consensus	(361)	Y V Y L T L C L S S L N S C I D P F V Y Y F A S E F Q L L C R				
Section 10						
	(406)	406	420	430	440	450
AAH18130_PAR1L	(366)	- - - - T V K Q M Q V S L T S K K H S R K S S S Y S S S S T T V K T S Y				
NP_001983_PAR1	(394)	- - - - P S S Y N S S G O E M A S K M D T C S S I N L N N S I Y K K L L T				
NP_835230_P2Y8	(316)	- - - - D G L D T R R E S L F S A R T T S V R S E A G A H P E @ M E G A T R P G L Q R Q E				
TransBD243560_HG52	(316)	- - - - D G L D T R R E S L F S A R T T S V R S E A G A H P E @ M E G A T R P G L Q R Q E				
NP_004092_PAR3	(375)	- - - -				
NP_005287_P2Y9	(334)	- - - - F K T E T P L T K P S L P A I Q E E V S D Q T T N N @ G E L M L E S T F				
P79928_XP2Y	(341)	R R C M H T N H P Q T E P H M T A G P L P V I S A E E I P S N @ S M V R D E N G E G S R E				
Consensus	(406)	T S L S A K S G				
Section 11						
	(451)	451	460	470	480	495
AAH18130_PAR1L	(398)	- - - -				
NP_001983_PAR1	(426)	- - - -				
NP_835230_P2Y8	(357)	S V F - - - -				
TransBD243560_HG52	(357)	S V F - - - -				
NP_004092_PAR3	(375)	- - - -				
NP_005287_P2Y9	(371)	- - - -				
P79928_XP2Y	(386)	H R V E W T D T K E I N Q M M N R R S T I K R N S T D K N D M K E N R H G E N Y L P Y V E				
Consensus	(451)	- - - -				
Section 12						
	(496)	496	510	520	530	540
AAH18130_PAR1L	(398)	- - - -				
NP_001983_PAR1	(426)	- - - -				
NP_835230_P2Y8	(360)	- - - -				
TransBD243560_HG52	(360)	- - - -				
NP_004092_PAR3	(375)	- - - -				
NP_005287_P2Y9	(371)	- - - -				
P79928_XP2Y	(431)	V V E K E D Y E T K R E N R K T T E Q S S K T N A E Q D E L Q T Q I D S R L K R G K W Q L				
Consensus	(496)	- - - -				

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	(541)	541	550	560	570	585	Section 13
AAH18130_PAR1L (398)		- - - - -					
NP_001983_PAR1 (426)		- - - - -					
NP_835230_P2Y8 (360)		- - - - -					
TransBD243560_HG52 (360)		- - - - -					
NP_004092_PAR3 (375)		- - - - -					
NP_005287_P2Y9 (371)		- - - - -					
P79928_XP2Y (476)	P79928_XP2Y (476)	S S K K G A A Q E N E K G H M E P S F E G E G T S T W N L L T P K M Y G K K D R L A K N V					
Consensus (541)							
	(586)	586	602				Section 14
AAH18130_PAR1L (398)		- - - - -					
NP_001983_PAR1 (426)		- - - - -					
NP_835230_P2Y8 (360)		- - - - -					
TransBD243560_HG52 (360)		- - - - -					
NP_004092_PAR3 (375)		- - - - -					
NP_005287_P2Y9 (371)		- - - - -					
P79928_XP2Y (521)	P79928_XP2Y (521)	E E V G Y G K E K E L Q N F P K A					
Consensus (586)							